

**Amendments to the Specification:**

Please replace the paragraph at page 15, lines 21-26 with the following amended paragraph:

The term "antibody" shall mean a polypeptide containing one or more domains capable of binding an epitope on an antigen of interest, where such domain(s) are derived from or homologous with the variable region of an antibody. Examples of antibodies include full length antibodies, antibody fragments, single chain molecules, bispecific or bifunctional molecules, diabodies, and chimeric antibodies (*e.g.* humanized and ~~Primatized~~<sup>TM</sup> PRIMATIZED<sup>TM</sup> antibodies). "Antibody fragments" include Fv, Fv', Fab, Fab', and F(ab')<sub>2</sub> fragments.

Please replace the paragraph at page 38, lines 1-11 with the following amended paragraph:

The effect of replacing residues on the polypeptide chain structure can be studied using a molecular graphics modeling program such as the ~~Insight~~<sup>TM</sup> INSIGHT<sup>TM</sup> program (Biosym Technologies). Using the program, those buried residues in the interface of the first polypeptide which have a small side chain volume can be changed to residues having a larger side chain volume (*i.e.* a protuberance), for example. Then, the residues in the interface of the second polypeptide which are in proximity to the protuberance are examined to find a suitable residue for forming the cavity. Normally, this residue will have a large side chain volume and is replaced with a residue having a smaller side chain volume. In certain embodiments, examination of the three-dimensional structure of the interface will reveal a suitably positioned and dimensioned protuberance on the interface of the first polypeptide or a cavity on the interface of the second polypeptide. In these instances, it is only necessary to model a single mutant, *i.e.*, with a synthetically introduced protuberance or cavity.